Amendments to the Specification:

Please amend the specification as follows.

1. Please delete the paragraph on page 38, starting at line 10 and continuing to line 25. This paragraph provides a description of Figure 8; however, there is no Figure 8 presented in the application.

2. Please replace the paragraph on page 41, starting at line 5, continuing to line 26 with the following rewritten paragraph:

Data acquisition, processing and analysis: Microarrays were scanned and analysed using a GenePix 4000A microarray scanner (Axon Instruments, Inc., Union City, N.J.), controlled by the software GenePix Pro 3.0 (Axon Instruments, Inc.). Individual data reports for all conducted experiments (including, e.g., median fluorescence intensities of all spots and local background) were exported and further analysed using the R software environment for statistical computing (~~http://www.r-projector.org~~) as well as Microsoft Excel 2000. Data sets for spots not recognized by the GenePix analysis Software were excluded from further considerations. Additionally, all remaining data sets were ranked according to spot homogeneity (as assayed by the ratio of median and mean fluorescence intensities), spot intensity and the standard deviation of log ratios for replicate spots. Those data points ranked among the lower 50%, and thus possessing the lower reliability based on the criteria just described, were eliminated. Data sets that could not be verified, either in a colour switch experiment (reversed assignment of fluorophores) or on a different experimental day, were omitted as well. For each hybridisation, fluorescence ratios (Cy5/Cy3) were normalized by variance stabilization (Huber, W., von Heydebreck, A., Sultmann, H., Poustka, A., and Vingron, M. 2002. Variance stabilization applied to microarray data calibration and to the quantification of differential expression. Bioinformatics, vol. 18, 96-104) or the median log ratio of all genes found in this ~~experiment In~~ <u>experiment. In</u> median log ratio normalization, accurate differential expression values for each gene were obtained by calculating the average of the normalized ratios of all independent hybridisations, successfully identifying that gene, and reversing the ratios from colour switch experiments prior to this operation.